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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 13:48:03 ; Search time 6978.47 seconds

(without alignments)
11880.962 Million cell updates/sec

Title: US-08-153-397A-1

Perfect score: 3962
Sequence: 1 CGGGCGCTGAGACTGGGCTGA.....AAAAAAAAAACCGAATTC 3962

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

- 1: gb_Da:*
- 2: gb_Htg:*
- 3: gb_In:*
- 4: gb_Om:*
- 5: gb_Ov:*
- 6: gb_Pat:*
- 7: gb_Ph:*
- 8: gb_Pl:*
- 9: gb_Pr:*
- 10: gb_Ro:*
- 11: gb_Stg:*
- 12: gb_Sy:*
- 13: gb_Un:*
- 14: gb_Vl:*
- 15: em_Da:*
- 16: em_Fun:*
- 17: em_Hum:*
- 18: em_In:*
- 19: em_Mu:*
- 20: em_Om:*
- 21: em_Or:*
- 22: em_Ov:*
- 23: em_Pat:*
- 24: em_Ph:*
- 25: em_Pl:*
- 26: em_Ro:*
- 27: em_Stg:*
- 28: em_Un:*
- 29: em_Vl:*
- 30: em_Htg_Hum:*
- 31: em_Htg_Inv:*
- 32: em_Htg_Other:*
- 33: em_Htgo_Inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description

1	3962	100.0	3962	6	I68738	
2	3625.6	91.5	3754	6	A42378	I68738 Sequence 1
3	3619.2	91.3	3738	6	HUMKRT	A42378 Sequence 1
4	3613.4	91.2	3849	9	BC008716	L11315 Homo sapien
5	3613.4	91.2	3849	9	BC013400	BC008716 Homo sapi
6	3544.4	89.5	3803	9	HUMKAK	BC013400 Homo sapi
7	3451	87.1	3637	6	AR094160	L20817 Homo sapien
8	3451	87.1	3637	6	AR103004	AR094160 Sequence
9	3451	87.1	3637	6	AR105288	AR103004 Sequence
10	3383.2	85.4	3554	6	AX268594	AR105288 Sequence
11	3383.2	85.4	3554	6	HSTRKE	180845 Sequence 3
12	3366	85.0	3841	9	HSTRKYK1	AX268594 Sequence
13	3312.2	83.6	3692	9	HOMCKA	X74979 H. sapiens T
14	3240.6	80.7	3659	10	AF026259	Z29093 H. sapiens T
15	2378.4	60.0	3674	10	MUSCAR	L57508 Homo sapien
16	2378.4	60.0	3743	10	RAPPTK3D	AF026259 Mus muscu
17	1192.2	30.1	1197	6	AR094162	L57509 Mus muscu
18	1192.2	30.1	1197	6	AR103006	L26525 Rattus norv
19	1192.2	30.1	1197	6	AR105290	AR094162 Sequence
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31	642	16.2	3157	6	I68739	X74764 H. sapiens m
32	642	16.2	3157	6	I68739	I68739 Sequence 3
33	639.8	16.1	3120	6	AR042425	I68740 Sequence 5
34	639.8	16.1	3120	6	AR054640	AR042425 Sequence
35	639.8	16.1	3259	10	MMTRYR10	AR054640 Sequence
36	639.8	16.1	3259	11	G49238	X76505 M. musculus
37	632.8	16.0	2521	10	AF329455	G49238 Ntrk3 Mous
38	608.2	15.4	349980	6	AX344571	AF329455 Crictulu
39	572	14.4	660	10	S77585	AX344571 Sequence
40	535.4	13.5	349980	6	AX344553	S77585 Plx-3l-radi
41	522.8	13.2	563	6	AX260854	AX344553 Sequence
42	394	9.9	400	11	G11190	AX260854 Sequence
43	362.4	9.1	175345	2	AC022301	G11190 SHGC-10808
44	362.4	9.1	203476	2	AC074150	AC022301 Mus muscu
45	341.6	8.6	349	10	S77556	AC074150 Mus muscu

ALIGNMENTS

RESULT	1					
LOCUS	I68738		3962 bp	DNA	linear	PAT 04-FEB-1998
DEFINITION	Sequence 1 from patent US 5677144.					
ACCESSION	I68738					
VERSION	I68738.1	GI:2830860				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 3962)					
AUTHORS	Ulrich, A. and Alves, F. Hildgaard, Elisabeth.					
TITLE	Recombinant DNA encoding CK 2, a receptor tyrosine Kinase					
JOURNAL	Patent: US 5677144-A 1 14-OCT-1997;					
FEATURES	Location/Qualifiers					
source	1..3962					
BASE COUNT	735 a 1234 c 1182 g 811 t					
ORIGIN						
Query Match	100.0%; Score 3962; DB 6; Length 3962;					
Best Local Similarity	100.0%; Pred. No. 0;					

	Matches	3962;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	CGGGCCCTGAGACTGGGGGTGACTGGAGCCTTAAGAGATTCCTGAGCTGGAGAGCCCGGACAG	60							
Db	1	CGGGCCTGAGACTGGGGGTGACTGGAGCCTTAAGAGATTCCTGAGCTGGAGAGCCCGGACAG	60							
QY	61	CTGCTTCGGGAGCCGCTCCCGACACCCGAGCCCGCGGCGCTCCCGCTCCCGCTCCCGGCTC	120							
Db	61	CTGCTTCGGGAGCCGCTCCCGACACCCGAGCCCGCGGCGCTCCCGCTCCCGCTCCCGGCTC	120							
QY	121	CGGGCTCTGGGCTCCCTCCGCGCTCCCGCGCGCTCCCGCGCGCTCCCGCGCGGAGAGGCCCGCT	180							
Db	121	CGGGCTCTGGGCTCCCTCCGCGCTCCCGCGCGCTCCCGCGCGCTCCCGCGCGGAGAGGCCCGCT	180							
QY	181	CCCGGGTCGGAGCGCTGGGTCTCCGGGAGAGCGATGAGAGTGTCTGAAGGTGGCTAT	240							
Db	181	CCCGGGTCGGAGCGCTGGGTCTCCGGGAGAGCGATGAGAGTGTCTGAAGGTGGCTAT	240							
QY	241	TCACGTAGCGATGGGGTGTGGACTTGAAGAAATGCCAAGATGCTGCCCAACCCCTTA	300							
Db	241	TCACGTAGCGATGGGGTGTGGACTTGAAGAAATGCCAAGATGCTGCCCAACCCCTTA	300							
QY	301	GGCCCGAGGGATCAGAGAGCTATGGGAGCCAGAGCCCTGATCTTACTGCTGCTGCT	360							
Db	301	GGCCCGAGGGATCAGAGAGCTATGGGAGCCAGAGCCCTGATCTTACTGCTGCTGCT	360							
QY	361	TGGTGCAAGTGGAGTCTGTACATGAAGAGGACATTTTATCTGTCGCAAGTCCCTATG	420							
Db	361	TGGTGCAAGTGGAGTCTGTACATGAAGAGGACATTTTATCTGTCGCAAGTCCCTATG	420							
QY	421	CCCTGGGCATGCAAGACCGGACCATCCAGACATGACATCTCTGCTTCAAGCTCTGT	480							
Db	421	CCCTGGGCATGCAAGACCGGACCATCCAGACATGACATCTCTGCTTCAAGCTCTGT	480							
QY	481	CAGATTCCACCTCCCGCCGCGCCAGACAGGTTGGAGACAGTACCGGGATGGGGCTGT	540							
Db	481	CAGATTCCACCTCCCGCCGCGCCAGACAGGTTGGAGACAGTACCGGGATGGGGCTGT	540							
QY	541	GCCCGCAGAGTCTGGTGTTCCTCAAGAGAGAGAGTACTTGCAGGTGATCTACAAACAC	600							
Db	541	GCCCGCAGAGTCTGGTGTTCCTCAAGAGAGAGAGTACTTGCAGGTGATCTACAAACAC	600							
QY	601	TCCACCTGGTGGCTCTGGTGGGACCCAGAGAGCGCATGCGGGGCGCTGGGCAAGAGT	660							
Db	601	TCCACCTGGTGGCTCTGGTGGGACCCAGAGAGCGCATGCGGGGCGCTGGGCAAGAGT	660							
QY	661	TCTCCCGAGCATACGGGCTGGGTACTCTCCCGGAGTGGTCCGCGTGGATGGGCTGGAAG	720							
Db	661	TCTCCCGAGCATACGGGCTGGGTACTCTCCCGGAGTGGTCCGCGTGGATGGGCTGGAAG	720							
QY	721	ACCAGTGGGGTTCAGAGAGTATCAGGCACATAGAGACCTGAGGGAGTGTGCTGAAG	780							
Db	721	ACCAGTGGGGTTCAGAGAGTATCAGGCACATAGAGACCTGAGGGAGTGTGCTGAAG	780							
QY	781	ACCTTGGGCCCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	840							
Db	781	ACCTTGGGCCCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	840							
QY	841	TGAGTGTCTGTGGGGGTGAGAGCTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	900							
Db	841	TGAGTGTCTGTGGGGGTGAGAGCTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	900							
QY	901	ACACGCGCCCTGTGGGGAGACAAATGTAATATCTGAGAGCCGTATACCTCAACGACTCA	960							
Db	901	ACACGCGCCCTGTGGGGAGACAAATGTAATATCTGAGAGCCGTATACCTCAACGACTCA	960							
QY	961	CCTATGAGGACATACCGTGGGAGAGTGCAGTATGGGGTCTGGGCCAGCTGAGCAGATG	1020							
Db	961	CCTATGAGGACATACCGTGGGAGAGTGCAGTATGGGGTCTGGGCCAGCTGAGCAGATG	1020							
QY	1021	GTGTGTGGGGGTGGATACCTTATGAGAGAGTCAAGAGACTCGGGTCTGGGCCAGCTTATG	1080							
Db	1021	GTGTGTGGGGGTGGATACCTTATGAGAGAGTCAAGAGACTCGGGTCTGGGCCAGCTTATG	1080							

QY	1081	ACTANGTGGATGAGACAAACACAGCTTCTCCAGTGGCTATGTGAGATGGAGTTGAGT	1140
Db	1081	ACTATGTGGATGAGACAAACACAGCTTCTCCAGTGGCTATGTGAGATGGAGTTGAGT	1140
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Db	1141	TTGACCGGCTAGAGGCTCTCCAGGCTATGCAAGTCCACTGTAAACATGACACAGCTGG	1200
QY	1201	GAGCCCGTCTGCGTGGCGGGGTGAAATGTGCTTCGGGCGTGGCCCTGCAATGGCTGGG	1260
Db	1201	GAGCCCGTCTGCGTGGCGGGGTGAAATGTGCTTCGGGCGTGGCCCTGCAATGGCTGGG	1260
QY	1261	AGGGGAGCCCATGCGGCACAACTAGGGGGCAACCTGGGGGACCCCAAGCGCGGGCTG	1320
Db	1261	AGGGGAGCCCATGCGGCACAACTAGGGGGCAACCTGGGGGACCCCAAGCGCGGGCTG	1320
QY	1321	TCTCAGTGCCTTGGGGGCGCGTGTGGCTTGCCTTTCGAGTAGTGCAGTCTCTCTTGGG	1380
Db	1321	TCTCAGTGCCTTGGGGGCGCGTGTGGCTTGCCTTTCGAGTAGTGCAGTCTCTCTTGGG	1380
QY	1381	GGCCCTGGTTACTTTACAGGAAATCTCTTCACTCTGATGTGGTGAACATTTCTCTC	1440
Db	1381	GGCCCTGGTTACTTTACAGGAAATCTCTTCACTCTGATGTGGTGAACATTTCTCTC	1440
QY	1441	CGGCACTGGAGAGCACTTCCCGACACCCCTGGTGGCGCGCTGGACCTCCACCA	1500
Db	1441	CGGCACTGGAGAGCACTTCCCGACACCCCTGGTGGCGCGCTGGACCTCCACCA	1500
QY	1501	ACTTCAGCAGCTTGAGCTGAGGCCAGAGCCAGCAGCCCTGGCCAAAGCCGAGGGGA	1560
Db	1501	ACTTCAGCAGCTTGAGCTGAGGCCAGAGCCAGCAGCCCTGGCCAAAGCCGAGGGGA	1560
QY	1561	GCCGCAACCGGCATCTGATGGGCGCTGGTGGGCATGACTCGTCTGCTGCTGCTCA	1620
Db	1561	GCCGCAACCGGCATCTGATGGGCGCTGGTGGGCATGACTCGTCTGCTGCTGCTCA	1620
QY	1621	TTGCCCTATGCTGTGGCGGCTGCACGTGGGCGCAGGCTCCTCAGCAAGGCTGAACGAGG	1680
Db	1621	TTGCCCTATGCTGTGGCGGCTGCACGTGGGCGCAGGCTCCTCAGCAAGGCTGAACGAGG	1680
QY	1681	TGTTGGGAAGAGAGACTAGAGGTTCCACTCTCTCTCCCTGGGACACTATCTCATCA	1740
Db	1681	TGTTGGGAAGAGAGACTAGAGGTTCCACTCTCTCTCCCTGGGACACTATCTCATCA	1740
QY	1741	ACCGCCAGGTCCTAGAGAGACCAACCCCGTACAGAGAGCCCGGCTCGTGGGAATCCG	1800
Db	1741	ACCGCCAGGTCCTAGAGAGACCAACCCCGTACAGAGAGCCCGGCTCGTGGGAATCCG	1800
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Db	1801	CCCACTCGGCTCTGTGTGCCAATBGTCTBGTGCTGCTCTCACAATCCAGCTAC	1860
QY	1861	GCTCTCTTGTGGCACTTACGGCCGTCGCCGTGAGAGCGCGGGGCCCCCAACCCGCT	1920
Db	1861	GCTCTCTTGTGGCACTTACGGCCGTCGCCGTGAGAGCGCGGGGCCCCCAACCCGCT	1920
QY	1921	GGGCGCAACCCACCAACCCAGGCTACAGTGGGACTATATGAGAGCTGAGAGCCAG	1980
Db	1921	GGGCGCAACCCACCAACCCAGGCTACAGTGGGACTATATGAGAGCTGAGAGCCAG	1980
QY	1981	GGCGCCCGCTTCTGCCCCCACTTCCCAAGAGCTCCCACTTATCCGAGGCTGACA	2040
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QY	2041	TTGTACCTCTGACAGGAGTACCGGGGGCAACACTATCTGTGCTGCATGCCCCAG	2100
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QY 3961 TC 3962
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RESULT 2
LOCUS A42378 3754 bp DNA linear PAT 06-MAR-1997
DEFINITION Sequence 1 from Patent WO9502187.
ACCESSION A42378
VERSION A42378.1 GI:2297854
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3754)
AUTHORS Gusterson,B.A., Crempston,M.R., Mitchell,P.J., Barker,K.T.,
Martindale,J.E., Page,M.J. and Spence,P.
TITLE CELL GROWTH FACTOR RECEPTORS
JOURNAL Patent: WO 9502187-A 1 19-JAN-1995;
COMMENT CANCER RES INST (GB)
FEATURES
source Other publication AU 7081094 950206.
1. 3754
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LBAFQAMQVHCNNMHTLGLARLPGVYECFRPRPAMAMEEPKHNHNGDPRARAY
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BASE COUNT 712 a 1146 c 1121 g 775 t
ORIGIN

Query Match 91.5%; Score 3625.6; DB 6; Length 3754;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 3733; Conservative 0; Mismatches 14; Indels 29; Gaps 7;

QY 181 CCGGGGCGAGCGCTGGGCTGCGCGGAGACGATGAGAGTGTCTGAAGTGTCTAT 240
DB 2 CCGGGGCGAGCGCTGGGCTGCGCGGAGACGATGAGAGTGTCTGAAGTGTCTAT 61
QY 241 TCACGTAGCGATGGGCTGACTTGAAGCATGCCAAGATGCTGCCACCCCTTA 300
DB 62 TCACGTAGCGATGGGCTGACTTGAAGCATGCCAAGATGCTGCCACCCCTTA 121
QY 301 GGGCCGAGGATCAGAGACTATGGACACGAGCCCTGTCTACTTACTGCTGCTCT 360
DB 122 GGGCCGAGGATCAGAGACTATGGACACGAGCCCTGTCTACTTACTGCTGCTCT 181
QY 361 TGTGTCAGATGAGATGCTGACATGAAGGACATTTGATCTCTGCAAGTGGCGGTATG 420
DB 182 TGTGTCAGATGAGATGCTGACATGAAGGACATTTGATCTCTGCAAGTGGCGGTATG 241
QY 421 CCCTGGGATGACGAGACCGGACCATCCAGACAGTACATCTCTGCTCCAGCTCTGCT 480
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DB 482 TCTCCCGGAGACTACCGGCTGCTTACTCCCGGAGTGTGTGGGCTGGAGGCTGAAGG 541
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QY 781 ACCCTGGGCCCCCAGATGTTGCCGACTGTTGCTTACCCCGCGGCTGACCGGGTCA 840
DB 602 ACCCTGGGCCCCCAGATGTTGCCGACTGTTGCTTACCCCGCGGCTGACCGGGTCA 661

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QY 1201 GAGCCGCTGTGCTGGCGGGGTGGAATGTGCTTCCGGCTGGCCCTGCCATGGCTGGG 1260
DB 1022 GAGCCGCTGTGCTGGCGGGGTGGAATGTGCTTCCGGCTGGCCCTGCCATGGCTGGG 1081
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RESULT 3
HUMRKT 3738 bp mRNA linear PRI 27-SEP-1993
LOCUS
DEFINITION Homo sapiens receptor tyrosine kinase mRNA, complete cds.
ACCESSION L11315
VERSION L11315.1 GI:403386
KEYWORDS receptor tyrosine kinase.
SOURCE Homo sapiens (library: lambda-gt11) term placenta cDNA to mRNA.
ORGANISM Homo sapiens

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Qy	1661	TGTTGGAAGAGAGCTGACGGTTACCTCTCTGTCCCTGGGGACACTATTCATCAACA	1740
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Qy	1741	ACCGCCCGGTCCTAGAGAGGACCCCCGTACAGAGACCCCCGCTGTGGAAATCCG	1800
Db	1562	ACCGCCCGGTCCTAGAGAGGACCCCCGTACAGAGACCCCCGCTGTGGAAATCCG	1621
Qy	1801	CCCACTCCGCTCCCTGTGTGCCCAATGGCTCTGGGTTGCTGTCTGCCAATCAGACTAC	1860
Db	1622	CCCACTCCGCTCCCTGTGTGCCCAATGGCTCTGGGTTGCTGTCTGCCAATCAGACTAC	1661
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Db	1682	GCCTCTCTTGTGGCCACTTACGCTGCCCCCTCGAGGACCAGGCCCCCACCACCGCT	1741
Qy	1921	GGGGCAAAACCCACAACCCAGGCCCTACAGTGGGGACTATATGAGCCTGAGAGCCAG	1980
Db	1742	GGGGCAAAACCCACAACCCAGGCCCTACAGTGGGGACTATATGAGCCTGAGAGCCAG	1801
Qy	1981	GCGCCCGGCTTGTGTGCCCACTCCCAAGAAACAGCTGCCCATATGACCTGAGAGCCAG	2040
Db	1802	GCGCCCGGCTTGTGTGCCCACTCCCAAGAAACAGCTGCCCATATGACCTGAGAGCCAG	1861
Qy	2041	TTGTTTACCTGCAAGGGGCGTCAACGGGGGCAACACTATGCTGTGCTGCACTGGCCCCAG	2100
Db	1862	TTGTTTACCTGCAAGGGGCGTCAACGGGGGCAACACTATGCTGTGCTGCACTGGCCCCAG	1921
Qy	2101	GGGAGTCGGGGGATGGGCCCCCAGAGTGGATTTCCCTCATCTCGACTCCGCTTCAGG	2160
Db	1922	GGGAGTCGGGGGATGGGCCCCCAGAGTGGATTTCCCTCATCTCGACTCCGCTTCAGG	1981
Qy	2161	AGAAGCTTGGCGAGAGGCGCACTTTGGGAGGTGCAACCTGTGAGTGGAGAGCCCTCAAG	2220
Db	1982	AGAAGCTTGGCGAGAGGCGCACTTTGGGAGGTGCAACCTGTGAGTGGAGAGCCCTCAAG	2041
Qy	2221	ATCTGGTCACTCTTGAATTTTCCCCCTTAATGTGGCTAAGGAGACCCCTTGCTGTAGCTG	2280
Db	2042	ATCTGGTCACTCTTGAATTTTCCCCCTTAATGTGGCTAAGGAGACCCCTTGCTGTAGCTG	2101
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RESULT 4
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 MGC:8681 IMAGE:2964574, mRNA, complete cds.
 ACCESSION BC008716
 VERSION BC008716.1 GI:14250529
 KEYWORDS MGC.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 3849)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAY-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 CONTACT: MGC help desk
 EMAIL: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CNA Library Preparation: Rubin Laboratory
 CNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/
 Contact: nisc.mgc@nih.gov
 Shevchenko, Y., Wetherby, R.D., Beckstrom-Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
 Lim, M., Maduro, O.L., Mastello, C., Mastrian, S.D., McLooney, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Stantirlop, S., Thomas, P.J.,
 Tjonson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov
 Series: IRAL Plate: 1 Row: 0 Column: 24
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 403386.
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 TNFSLLEPRLQOOPVAKAESPRALLIGCVAILILLILLIAMLRLHRLRLSLKA
 ERYLLEELIYHLSVPGDTILLNNRPGREPPVOEPFRNPNAPCVNSAYSG
 DYMEKPGALPLPPPNPSVPHLEADIVLQVGTGNTAVPALPGAGADPPRY
 DFPRLRFKFEKLEGOFEVHLCEVDSPODLSDPLNRYKHPLIVAVKILRPDA
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 FTIKIADFGMSRNLXAGDYRVOGRALPITNMAECLIMKFTTASVAFYTLIRE
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BASE COUNT 715 a 1181 c 1165 g 788 t
 ORIGIN

Query Match 91.2% Score 3613.4 DB 9; Length 3849;
 Best Local Similarity 95.9% Pred. NO. 0;
 Matches 3792; Conservative 0; Mismatches 31; Indels 130; Gaps 3;

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 Db 24 GGCCCTGAGCGGAGCTGACGACGACCCCTGGGGCCAGCTTTGAGAGCCCCGACAGC 83
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DEFINITION Homo sapiens, clone MGC:3909 IMAGE:2964574, mRNA, complete cds.
ACCESSION BC013400
VERSION BC013400.1 GI:15426562
KEYWORDS MGC.
SOURCE human.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3849)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
Contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahney, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 10 Row: f Column: 21
This clone was selected for full length sequencing because it
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FEATURES

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CDS

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ORIGIN

Query Match 91.2%; Score 3613.4; DB 9; Length 3849;
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RESULT 6
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 LOCUS HUMCAK 3803 bp mRNA linear PRI 11-MAY-1994
 DEFINITION Homo sapiens tyrosine protein kinase (CAK) gene, complete cds.
 ACCESSION L20817.1 GI:306474
 VERSION 1
 KEYWORDS A5-antigen; factor V; factor VIII; tyrosine protein kinase.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Perez, J.L., Shen, X., Finkernagel, S., Sciorra, L., Jenkins, N.A., Gilbert, D.J., Copeland, N.G. and Wong, T.W.
 TITLE Identification and chromosomal mapping of a receptor tyrosine kinase with a putative phospholipid binding sequence in its ectodomain
 JOURNAL Oncogene 9, 211-219 (1994)
 MEDLINE 94134417
 REFERENCE 2 (bases 1 to 3803)
 AUTHORS Johnson, U.D.
 TITLE Direct Submission
 JOURNAL Submitted (17-FEB-1993) J.D. Johnson
 REFERENCE 3 (sites)
 AUTHORS Johnson, J.D., Edman, J.C. and Rutter, W.J.
 TITLE A receptor tyrosine kinase found in breast carcinoma cells has an extracellular discoidin I-like domain
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 5677-5681 (1993)
 MEDLINE 93296201
 REFERENCE 4 (sites)
 AUTHORS Wong, T.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-1993) T. Wong
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LOCUS	AR094160	3637 bp	DNA	linear	PAT 08-SEP-2000
DEFINITION	Sequence 3 from patent US 6001621.				
ACCESSION	AR094160				
VERSION	AR094160.1	GI:10020905			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 3637)				
TITLE	Godowaki, P.J., Mark, M. R. and Scadden, D. T.				
JOURNAL	Protein tyrosine kinases				
FEATURES	Patent: US 6001621-A 3 14-DEC-1999;				
	Location/Qualifiers				
	1..3637				
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Query Match	87.1%;	Score 3451;	DB 6;	Length 3637;
Best Local Similarity	97.0%;	Pred. No. 0;		
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QY 2536 CGCAGGGGGCCACCATGACTACCAATGCTGTGCTGATGTGGCAGCCAGATCCCTCGC 2595
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Db 2639 TCATCGAGAACGCGGGGAGATTCTTCGGGAGCAAGGCGCGCAGAGTGTACCTGTCCGGC 2698
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RESULT 8
ARI03004 3637 bp DNA linear PART 14-FEB-2001
LOCUS ARI03004
DEFINITION Sequence 3 from patent US 6087144.

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QY	1096	GCAACACACAGCTTCTCCAGTAGGATGAGAGATGGAGTTTGAATTGACCGGCGAGAGG	1155
Db	857	GCAACACACAGCTTCTCCAGTAGGATGAGAGATGGAGTTTGAATTGACCGGCTGAGAGG	916
QY	1156	CCCTTCAGGCTATGCAAGGTCACATGTAAACAATGCACAGCGTGGAGAGCCGCTGCCTG	1215
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QY	1216	GGGGGGTGGAAATGTGCTCTCCGGGCTGGCCCTGCATGGCTGGAGGGAGAGCCCATGC	1275
Db	977	GGGGGGTGGAAATGTGCTCTCCGGGCTGGCCCTGCATGGCTGGAGGGAGAGCCCATGC	1038
QY	1276	GGCACACCTTAGGGGGGCAACCTGGGGGGAGCCCGACAGAGCGGGGCTGCTAGTGGCCCTTG	1335
Db	1037	GGCACACCTTAGGGGGGCAACCTGGGGGGAGCCCGACAGAGCGGGGCTGCTAGTGGCCCTTG	1096
QY	1336	GGGGCCGTGTGGCTGCTTTCGTGCAAGTGCAGTCCGCTCTCTTGGGGGGCCCTGGTACTCT	1395
Db	1097	GGGGCCGTGTGGCTGCTTTCGTGCAAGTGCAGTCCGCTCTCTTGGGGGGCCCTGGTACTCT	1156
QY	1396	TGAGGGAATCTCCTCATCTCTATGTGTGAACAATTCCTCTCCGCACTGGAGGCA	1455
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Db	1217	CCCTCCGCGCGAGCCGCCCTGGGGGGCGGCGTGGGCCACCTCCACACAATTCAGACACTTGG	1276
QY	1516	AGCTGGAGCCCAAGAGGCGCAGAGCCCTGTGCCAAGGCGCAGAGGGAGACCCGACCGCATCC	1575
Db	1277	AGCTGGAGCCCAAGAGGCGCAGAGCCCTGTGCCAAGGCGCAGAGGGAGACCCGACCGCATCC	1336
QY	1576	TCATGTGCTGCCCTGGTGCCATCATCTGCTCTGCTGCTCATCATGTCCTCATGCTCT	1635
Db	1337	TCATGTGCTGCCCTGGTGCCATCATCTGCTCTGCTGCTCATCATGTCCTCATGCTCT	1396
QY	1636	GGCGGCTCAGTGGCGGAGGCTGCTCTGCAAGGCTCAAGGAGGGTGTGGAAAGAGAGC	1695
Db	1397	GGCGGCTCAGTGGCGGAGGCTGCTCTGCAAGGCTCAAGGAGGGTGTGGAAAGAGAGC	1456
QY	1696	TGACGGTTCACCTCTGTCTGTCGCTGGGGAGACATATCTCATCAACAACCGCCAGAGTCTA	1755
Db	1457	TGACGGTTCACCTCTGTCTGTCGCTGGGGAGACATATCTCATCAACAACCGCCAGAGTCTA	1516
QY	1756	GAGAGCCACCCCGTACCAAGAGCCCGGCGCTGTGGGAATCGGCCCACTCGCTCCT	1815
Db	1517	GAGAGCCACCCCGTACCAAGAGCCCGGCGCTGTGGGAATCGGCCCACTCGCTCCT	1576
QY	1816	GGTGGCCCAATGGGCTGGGTGGTGGTGTCTCCAAATCCACCTACCGGCTCTTGTGGCA	1875
Db	1577	GGTGGCCCAATGGGCTGGGTGGTGGTGTCTCCAAATCCACCTACCGGCTCTTGTGGCA	1636
QY	1876	CTTACGCCCTGCCCTTCGAGAGCCCGGAGCCCGCCACACCGCGCTGGGCGCAACCCACCA	1935
Db	1637	CTTACGCCCGTCCCCCTTCGAGAGCCCGGAGCCCGCCCGCCACACCGCGCTGGGCGCAACCCACCA	1696
QY	1936	ACACCCAGGCTTACATGTGGGACTATATGAGAGCTGAGAGCCAGAGCCCGCGCTTGTGC	1995
Db	1697	ACACCCAGGCTTACATGTGGGACTATATGAGAGCTGAGAGCCAGAGCCCGCGCTTGTGC	1756
QY	1996	CCCCACCTCCCGCAAGAGGCTCCCCCATTTATGCGAGGCTGACATTTTACCTCGAGG	2055
Db	1757	CCCCACCTCCCGCAAGAGGCTCCCCCATTTATGCGAGGCTGACATTTTACCTCGAGG	1816
QY	2056	GGCTACACGGGGGCAACACTTATGTGCTGCCTGCACCTGCCCCAGGGGCACTGGGGATG	2115
Db	1817	GGCTACACGGGGGCAACACTTATGTGCTGCCTGCACCTGCCCCAGGGGCACTGGGGATG	1876
QY	2116	GGGCCCCAGATGGATTTCCTCATGTCACTCCGCTTCAAGAGAGATGTGGGAGG	2175

Db	1877	GGCCCCCAGAGTGGATTTCCTCGATCTCGATCCGGCTTCAAGGAGAAAGCTTGCGAGG	1936
QY	2176	GCACGTTTGGGAGAGTCCACCTGTGTGAGGTGCACAGCCCTCAAGATCTGGTCAATCTTG	2233
Db	1937	GCACGTTTGGGAGAGTCCACCTGTGTGAGGTGCACAGCCCTCAAGATCTGGTCAATCTTG	1998
QY	2236	ATTTCGCCCTTAATGTCTGTAAAGGACACCCCTTGGTGTACTGTGCAGAACTTCAAGCG	2295
Db	1997	ATTTCGCCCTTAATGTCTGTAAAGGACACCCCTTGGTGTACTGTGCAGAACTTCAAGCG	2056
/ QY	2236	CAGATGCCACCAAGATATGCCAGCTTCTCTTCTCCAGAAATATTTCTGAAGAGG	2355
Db	2057	CAGATGCCACCAAGAAATG-----CCAGAAATGATTTCTGAAAGAGG	2098
QY	2356	TGAAGATCATGTGGAGGCTCAAGAGCCCAACATCATTTGGCTGTGGGCGGTGTGTGC	2415
Db	2099	TGAAGATCATGTGGAGGCTCAAGAGCCCAACATCATTTGGCTGTGGGCGGTGTGTGC	2158
QY	2416	AGGACGACCCCTCTGTGATGATTACTGACTACATGTAGAGAACGGCAGCTCAACAGTATCC	2475
Db	2159	AGGACGACCCCTCTGTGATGATTACTGACTACATGTAGAGAACGGCAGCTCAACAGTATCC	2218
QY	2476	TCAATGCCCAACAGTCTGAGAGAAAGGACGCGAGGGGGCCCTTGGGAGCGGCAAGCTG	2535
Db	2219	TCAATGCCCAACAGTCTGAGAGAAAGGACGCGAGGGGGCCCTTGGGAGCGGCAAGCTG	2278
QY	2536	CGCAGGGGGCCACCATCAGCTACCAATCTGCTGTGATGTGGCAGCCAGATCGCATCGG	2595
Db	2279	CGCAGGGGGCCACCATCAGCTACCAATCTGCTGTGATGTGGCAGCCAGATCGCATCGG	2388
QY	2596	GCATGCCCTATCTGGCCACACTAATCTTGTACATCGGGAAGTGGCCACAGCGGAATCTCC	2655
Db	2339	GCATGCCCTATCTGGCCACACTAATCTTGTACATCGGGAAGTGGCCACAGCGGAATCTCC	2398
QY	2656	TAGTGGGGGAAAATTTACACATCAAAATGCGAGACTTGGATGTAGCGGGAACCTATATG	2715
Db	2399	TAGTGGGGGAAAATTTACACATCAAAATGCGAGACTTGGATGTAGCGGGAACCTATATG	2488
QY	2716	CTGGGGACATTTACCGTGTGCAGGGCCGGGACAGTGTGCCATCCATCGGTAGTGGCTGGG	2775
Db	2459	CTGGGGACATTTACCGTGTGCAGGGCCGGGACAGTGTGCCATCCATCGGTAGTGGCTGGG	2518
QY	2776	AGTCAATCCATCAGGGGGAATTTAGACATCGGAGTGAAGCTGTGGGCACTTGGTGTGACCC	2835
Db	2519	AGTCAATCCATCAGGGGGAATTTAGACATCGGAGTGAAGCTGTGGGCACTTGGTGTGACCC	2578
QY	2836	TGTGGAGGTGTGATGCTGTGTAGGGCCAGCCCTTGGGAGGTCAACGACGACGACG	2895
Db	2579	TGTGGAGGTGTGATGCTGTGTAGGGCCAGCCCTTGGGAGGTCAACGACGACGACG	2638
QY	2896	TCAATCGGAACCGGGGGGAGTTTTCGGGAGACAGGGCCGCGAGTGTACCTGTCCGGC	2955
Db	2639	TCAATCGGAACCGGGGGGAGTTTTCGGGAGACAGGGCCGCGAGTGTACCTGTCCGGC	2698
QY	2956	CGCCTCGCTCCCGCAGGGGCTTATATGACTGTATGCTTGGGTGTGGAGCCGGGAGTGTG	3015
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QY	3016	AGCAGGACACCCCTTTCCCAAGCTGCATCGGTTCTCTGGCAGAGGATGACTCAACAGG	3075
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QY	3136	CTAAACACAGAGACAAATGGCACTCTGCCCTTCCCTCCCGACAGCCCATACGCT	3195
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[illegible]

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DEFINITION	Sequence 3 from patent US 6096527.			PAT 14-FEB-2001
ACCESSION	AR105288			
VERSION	AR105288.1	GI:12818865		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 3637)			
TITLE	Godowski, P.J., Mark, M.R. and Scadden, D.T.			
JOURNAL	Nucleic acids encoding protein tyrosine kinases			
FEATURES	Patent: US 6096527-A 3 01-AUG-2000;			
Source	Location/Qualifiers			
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	/organism="unknown"			
BASE COUNT	721 a	1094 c	1079 g	743 t
ORIGIN				

QY 2416 AGAGAGACCCCTCTGATGATTTACTGACTATGAGAGAGGCGACCTCAACAGTTC 2475
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 VERSION I80845.1 GI:3209135
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 3637)
 AUTHORS Godowski,P.J., Mark,M.R. and Seadden,D.T.
 TITLE Antibodies specific for Rse receptor protein tyrosine kinase
 JOURNAL Patent: US 5709858-A 3 20-JAN-1998;
 FEATURES
 source 1..3637
 BASE COUNT 721 a 1094 c 1079 g 743 t
 ORIGIN

Query Match 87.1%; Score 3451; DB 6; Length 3637;
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OY	556	TGTTTCCCAAGAGAGAGAGACTTGGAGAGTGATCTCAACAGACTCAACCTGTGGTGC	615
Db	317	TGTTTCCCAAGAGAGAGAGACTTGCAGAGTGGATCTCAACAGACTGCACCTGTGTGC	376
OY	616	TGGTGGCACCACAGGAGCAGCATGCGGGGGCTGGGCAAGAGATTCCCGAGCTAC	675
Db	377	TGGTGGGACCCACAGGAGCAGCATGCGGGGGCTGGGCAAGAGATTCTCCCGAGCTAC	436
OY	676	GGCTCGTTACTCCCGGGATGGTGGCGGTGAGTGGGTGGGAAGAGACCGTGGGTCAAG	735
Db	437	GGCTCGTTACTCCCGGGATGGTGGCGGTGAGTGGGTGGGAAGAGACCGTGGGTCAAG	496
OY	736	AGTGATCTCAGGCACATGAGACCTTAGAGGAGTGGTGTGAAGAGACTTGGGCCCCCA	795
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OY	1096	GCAACACAGCTTCTCCAGTGGCTATGTGGAATGAGATTGACTTGAACCGGCTGAGGG	1155
Db	857	GCAACACAGCTTCTCCAGTGGCTATGTGGAATGAGATTGACTTGAACCGGCTGAGGG	916
OY	1156	CCTTCACAGGCTATCAGAGTCCACTGTAAACAATGACACCGTGGGAGCGGTGCGCTG	1215
Db	917	CCTTCACAGGCTATCAGAGTCCACTGTAAACAATGACACCGTGGGAGCGGTGCGCTG	976
OY	1216	GGGGGTGGAATGTGCTTCGCGCGTGGCCCTGACCATGGGCTGGGAGGGGAGCCCATGC	1275
Db	977	GGGGGTGGAATGTGCTTCGCGCGTGGCCCTGACCATGGGCTGGGAGGGGAGCCCATGC	1036
OY	1276	GCCACAACCTAGGGGGGCAACCTGGGGGAGCCCAACCCGGGGCTGTCTACAGTCCCCCTG	1335
Db	1037	GCCACAACCTAGGGGGGCAACCTGGGGGAGCCCAACCCGGGGCTGTCTACAGTCCCCCTG	1096
OY	1336	GGGCGCTGTGGCTCGCTTCTGACAGTGCCTCTCTTTCGGGGCCCTGGTACTCT	1395
Db	1097	GGGCGCTGTGGCTCGCTTCTGACAGTGCCTCTCTTTCGGGGCCCTGGTACTCT	1156
OY	1396	TCACGGAATCTCCTTCATCTCTGATGTGTGAACAATTCTCTCCGACACTGGAGGACA	1455
Db	1157	TCACGGAATCTCCTTCATCTCTGATGTGTGAACAATTCTCTCCGACACTGGAGGACA	1216
OY	1456	CCTTCGCGCAGCCCTGTGTGGCGGCTGGGCCACCTCCCAACAATTCAAGAGCTGG	1515
Db	1217	CCTTCGCGCAGCCCTGTGTGGCGGCTGGGCCACCTCCCAACAATTCAAGAGCTGG	1276
OY	1516	AGCTGAGCCCAAGAGGCAAGCCCGGTGGCCAAGGCCAGAGGGAGCCCAAGCCCATCC	1575
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[illegible]

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OY	2716	CTGGGGACTATTACCGTGTGACAGGGCCGGGCAATGCTGCCAATCCGCTGGATAGGCGCTGG	2775
Db	2459	CTGGGGACTATTACCGTGTGACAGGGCCGGGCAATGCTGCCAATCCGCTGGATAGGCGCTGG	2518
OY	2776	AGTGCATCCTCATGGGGAGTTGCACGACTGCGAGTACGTATGGGCGCTTTGGTGTGACCC	2835
Db	2519	AGTGCATCCTCATGGGGAGTTGCACGACTGCGAGTACGTATGGGCGCTTTGGTGTGACCC	2578
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Db	2579	TGTGGAGGTCTCTATCTCTGTAGGGCCAGCCCTTGGGAGCTCACCGACGACAGG	2638
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OY	2956	CGCTGCGCTGCCGACAGGCCCTATATGAGCTGATGCTTGCTGTGAGCGGAGGTG	3015
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OY	3016	AGCAGCGACACACCTTTTCCCACTGCAATCGTGTCTGTGGCAAGAGATGACTCAACAGG	3075
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OY	3436	ACTGGACAACTGATTCCTCGAGAGGTGGCTGG-CCCAAGCTTCTCTCCCTGTAC	3494
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RESULT 11

LOCUS	AX268594	3554 bp	DNA	linear	PAT 29-OCT-2001
DEFINITION	Sequence 13 from Patent WO0175440.				
ACCESSION	AX268594				
VERSION	AX268594.1	GI:16541709			
KEYWORDS					

SOURCE

ORGANISM

REFERENCE
1 (sites)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

TITLE	Fractalkine
JOURNAL	Schizophrenia related genes
	Patent: WO 0175440-A 13 11-OCT-2001
	WELEFIDE CORPORATION (US)

FEATURES	LOCATION/QUALIFIERS
source	1. .3554

BASE COUNT	682 a	1064 c	1065 g	743 t
ORIGIN	/organism="Homo sapiens" /db_xref="taxon:9606"			

Query Match: 85.4%; Score 3383.2; DB 6; Length 3554;

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Best Local Similarity 96.4%; Pred. No. 0;
Matches 3545; Conservative 0; Mismatches 3; Indels 130; Gaps 3;

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Db 62 TGTCACTTAACTGGCTGCTCTCTTGGTGGCAAGTGGAGATGCTGCATGAAAGGACATT 121

QY	397	122	Db
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b		
OY		

[illegible]

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[illegible]

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Db	2573	TATATAGCTGATGTCCTTGCTGGAGCCGGGAGTCTGAGCAGGACACCATCTTTCC	2632
OY	3037	AGCTGCATCGGTTCTCCTGGAGAGATGACATAACAAGSTGTGAATCACATCTCAGCTG	3096
Db	2633	AGCTGCATCGGTTCTCCTGGAGAGATGACATAACAAGSTGTGAATCACATCTCAGCTG	2692
OY	3097	CCCCCTCCCTCAGGAGATGATCCAGAGGGAAAGCCAGTAGACTATAAACAAGAGACCAATG	3156
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RESULT	LOCUS	DEFINITION	ACCESSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source
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		X74979										
		X74979.1 GI:400462										
		trk E gene; trk E protein.										
		human.										
		Homo sapiens										
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		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.										
		1 (bases 1 to 3554)										
		Di Marco, E., Cuttilli, N., Guerra, L., Cancedda, R. and De Luca, M.										
		Molecular cloning of trke, a novel trk-related putative tyrosine										
		kinase receptor isolated from normal human keratinocytes and widely										
		expressed by normal human tissues										
		J. Biol. Chem. 268 (32), 24290-24295 (1993)										
		94043265										
		2 (bases 1 to 3554)										
		De Luca, M.										
		Direct Submission										
		Submitted (08-SEP-1993) M. De Luca, Istituto Nazionale per la										
		Ricerca sul Cancro, Lab Differenziamento Cellulare, Viale										
		Benedetto XV, 10 - 16132 Genova, ITALY										
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U29093

VERSION

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KEYWORDS

receptor tyrosine kinase.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 3841)

AUTHORS

Laval, S., Butler, R., Shelling, A.N., Hanby, A.M., Poulson, R. and Ganesan, I. S.

JOURNAL

Isolation and characterization of an epithelial-specific receptor tyrosine kinase from an ovarian cancer cell line

MEDLINE

95151638

REFERENCE

2 (bases 1 to 3841)

AUTHORS

Shelling, A.N., Butler, R., Jones, T., Laval, S., Boyle, J.M. and Ganesan, I. S.

JOURNAL

Localization of an epithelial-specific receptor kinase (EDDR1) to chromosome 6q16

TITLE

Genomics 25 (2), 584-587 (1995)

JOURNAL

95309932

REFERENCE

3 (bases 1 to 3841)

AUTHORS

Kedinger, C.

JOURNAL

Direct Submision

TITLE

Submitted (17-DEC-1993) Claude Kedinger, CNRS Laboratoire de genétique moléculaire-U184, INSERM, 11, rue Humann, Strasbourg, Alsace, 67085 cedex, FRANCE

FEATURES

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QY	2677	TCAAAATCGGACACTTTGGCATGAGCCGGAACCTTATGCTGGGACTATTAACGCTGTC	2736
Db	2564	TCAAAATCGGACACTTTGGCATGAGCCGGAACCTTATGCTGGGACTATTAACGCTGTC	2623
QY	2737	AGGGCGGGGACAGTGCATCCGTCGCTGGATGGGCTGGGAGTGCATCTCATGGGGAGT	2796
Db	2624	AGGGCGGGGACAGTGCATCCGTCGCTGGATGGGCTGGGAGTGCATCTCATGGGGAGT	2683
QY	2797	TCAAGATGCGGATGACGTGTGGGACCTTTGGGTGTACACCTGTGGGAGGTGTGTATGCTCT	2856
Db	2684	TCAAGATGCGGATGACGTGTGGGACCTTTGGGTGTACACCTGTGGGAGGTGTGTATGCTCT	2743
QY	2857	GTAAGGCCACAGCCCTTTGGGACACTCACCGACGACAGCTCATCGAGAACGCGGGGAGT	2916
Db	2744	GTAAGGCCACAGCCCTTTGGGACACTCACCGACGACAGCTCATCGAGAACGCGGGGAGT	2803
QY	2917	TCTTCCGGGACCAAGGGCCGGGAGGTATACCTGTCCCGGCCCTGCTGCTCCCGGAGGCC	2976
Db	2804	TCTTCCGGGACCAAGGGCCGGGAGGTATACCTGTCCCGGCCCTGCTGCTCCCGGAGGCC	2863
QY	2977	TATATGAGCGATGATCGGTGCTGTGGAGCGGGAGTCTGACACAGGACACACCTTTTCCC	3036
Db	2864	TATATGAGCGATGATCGGTGCTGTGGAGCGGGAGTCTGACACAGGACACACCTTTTCCC	2923
QY	3037	AGCTGCATCGGTTCTGTGCGAGAGATGCATCAACAGGTTGTGATCACAATCAACTG	3096
Db	2924	AGCTGCATCGGTTCTGTGCGAGAGATGCATCAACAGGTTGTGATCACAATCAACTG	2983
QY	3097	CCCTCCCTTCAGGGAATGATCCAGGGGAAAGCCAGTGAACACTTAAACAAGAGACACATG	3156
Db	2984	CCCTCCCTTCAGGGAATGATCCAGGGGAAAGCCAGTGAACACTTAAACAAGAGACACATG	3043

QY	3157	GCACCTGACCCCTTCCCTCCGCGGACAGCCCATACCTCTTAATAAGAGGAGTAGACTGCA	3216
Db	3044	GCACCTTGCCCTTCCCTCCGCGGACAGCCCATACCTCTTAATAAGAGGAGTAGACTGCA	3103
QY	3217	GGTGGGCTGGGGCCACCCAGGAGGAGCTGATGAGCCCTCTTCCCTCTCTGAGACACTGTCA	3276
Db	3104	GGTGGGCTGGGGCCACCCAGGAGGAGCTGATGAGCCCTCTTCCCTCTCTGAGACACTGTCA	3163
QY	3277	TGTCCCTTCTCTGTTCTTCTTCTTCTTAAGAG--CCCTGTGCGCCACCCAGCTGTCTGT	3334
Db	3164	TGTCCCTTCTCTGTTCTTCTTCTTCTTAAGAGAGCCCTGTGCGCCACCCAGCTGTCTGT	3223
QY	3335	GGATGGATGCTCTCCACCCCTCTAGCATCCCTTGGGGAAAGGTTGGGGAGTAATATA	3394
Db	3224	GGATGGATGCTCTCTCACCCCTCTTAGCATCCCTTGGGGAAAGGTTGGGGAGTAATATA	3283
QY	3395	GGATAGACACTGGACATGAGCCATTGAGACACTGTGGGCCCCACTGGAGAACACTGATTC	3454
Db	3284	GGATAGACACTGGACATGAGCCATTGAGACACTGTGGGCCCCACTGGAGAACACTGATTC	3343
QY	3455	TGGAGAGTGGCTGCG--CCCCAGCTTCTCTCTCCCTGTACACACTGGACCCCACTGGCT	3513
Db	3344	TGGAGAGTGGCTGCGCCCCAGCTTCTCTCTCCCTGTACACACTGGACCCCACTGGCT	3403
QY	3514	GAGATCTGGGGGGTAGAGAGGACAGAGAGAGAGAAATGTTCTCTTGTGCTCTCTCT	3573
Db	3404	GAGATCTGGGGGGTAGAGAGGACAGAGAGAGAGAAATGTTCTCTTGTGCTCTCTCT	3463
QY	3574	GTACTTGTCTCAGCTTGGGCTTCTCTCTCCCTCCTACACTGTAACACTGGACCTGGGG	3633
Db	3464	GTACTTGTCTCAGCTTGGGCTTCTCTCTCCCTCCTACACTGTAACACTGGACCTGGGG	3523
QY	3634	TAGCCCCGCCAGCCCTCAGTACCCCACTTCCCACTTGCACTGTGTAGCTAGAACT	3693
Db	3524	TAGCCCCGCCAGCCCTCAGTACCCCACTTCCCACTTGCACTGTGTAGCTAGAACT	3583
QY	3694	TCTTAACCTTAACCTTCTGTGGAGTAATATTTGGGATTGGGGGAAAGGGAGAGAA	3753
Db	3584	TCTTAACCTTAACCTTCTGTGGAGTAATATTTGGGATTGGGGGAAAGGGAGAGAA	3643
QY	3754	CGGCCCATAGCCCTGGGGTTGGACATCTCTAGTAGCTGCACATGATTTTCTATATA	3813
Db	3644	CGGCCCATAGCCCTGGGGTTGGACATCTCTAGTAGCTGCACATGATTTTCTATATA	3703
QY	3814	TCACTTGGGGTTTGTACATTTTGGGGGAGAGACACAGATTTTAACTAATATATGGA	3873
Db	3704	TCACTTGGGGTTTGTACATTTTGGGGGAGAGACACAGATTTTAACTAATATATGGA	3763
QY	3874	CCTAGCTTGAGGCAATTTTAAATCCCTCCTAGCTAGGACAGTAAATAAGTTGAGTTT	3933
Db	3764	CCTAGCTTGAGGCAATTTTAAATCCCTCCTAGCTAGGACAGTAAATAAGTTGAGTTT	3823
QY	3934	CCACAAAAAAAAAAAAAAAAA 3951	
Db	3824	CCACAAAAAAAAAAAAAAAAA 3841	
RESULT	14		
LOCUS	HUMCAKA	3692 bp	linear
DEFINITION	Homo sapiens Cak receptor kinase mRNA, complete cds.		PRI 31-JUL-1996
ACCESSION	L57508		
VERSION	L57508.1	GI:1160924	
KEYWORDS	receptor kinase.		
SOURCE	Homo sapiens lung CDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotic: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo. 1 (bases 1 to 3692)		
AUTHORS	Perez,J.L., Jing,S.O. and Wong,T.W.		
TITLE	Identification of two isoforms of the Cak receptor kinase that are coexpressed in breast tumor cell lines		

Db 1502 TGCTGCGGGCTGCACCTGGCCAGGCTCTCTACGACGAGCTGAACGAGGCTGTGGAAAG 1561
QY 1690 AGGAGCTGACGGCTTCACTCTCTGTCCCTGGGAGACATATCTCATCAACAACCGCCAG 1749
Db 1562 AGGAGCTGACGGCTTCACTCTCTGTCCCTGGGAGACATATCTCATCAACAACCGCCAG 1621
QY 1750 GTCTTAGAAGACCCCGGTACACGAGACCCCGGCTGTGGAAATCCGCCACTCCG 1809
Db 1622 GTCTTAGAAGACCCCGGTACACGAGACCCCGGCTGTGGAAATCCGCCACTCCG 1681
QY 1810 CTCCCTGTCCCAATGAGCTGTGGCTGTCTCTCAATCCAGCTACCGCTCTCCCTTC 1869
Db 1682 CTCCCTGTCCCAATGAGCTGTGGCTGTCTCTCAATCCAGCTACCGCTCTCCCTTC 1704
QY 1870 TGGCCACTTACGCGGTCCCTCGAGGCCCGGCCCCACACCGGCTGGCCAAAC 1929
Db 1705 ----- 1704
QY 1930 CCACCAACCCAGGCTTACATGAGGAGCTATATGAGGCTTAGAAGCCAGGCCCGCC 1989
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QY 1990 TTCTGCCCCACCTCCCGGAGAGGTCCTCCATTATGCGAGGCTGACATTTACCC 2049
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QY 2290 TACGGCCAGATGCCCAAGATGCGAGCTTCTGTCTCCAGGATGATTTCTTGA 2349
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QY 2410 GTGTGACAGACGACCCCTCTGTCATGATTAATGACTACATGAGAAAGGCGACTCAAC 2469
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Db 2633 AGCAGGTCAATGAGAACGGGGGGAGTCTTCCGGAGACAGGCGCGGAGCTTACTCT 2692
QY 2950 CCCGGCGGCTGCTGCCCCGAGGCGCTATGAGCTGATGCTTGGTCTGAGGCGG 3009
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QY 3550 AAATTTCTTCTGCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3609
Db 3283 AAATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3342
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QY 3730 GGATTGGGGGGAAGAGGAG 3789
Db 3461 GGATTGGGGGGAAG 3519
QY 3790 GCTGCACTGATTTTCTTAATCACTTGGGGGTGATTAATTTTGGGGGAGAGAGAGAGAG 3849
Db 3520 GCTGCACTGATTTTCTTAATCACTTGGGGGTGATTAATTTTGGGGGAGAGAGAGAGAGAG 3579

[illegible]

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Qy	2371	GGCTCAAGGACCCCAATCATTTGGGTGGGGCGGTGTGAGGACGACCCCT	2430	
Db	2127	GGCTAAGAGACCCCAACATCTATCCGGCTCTCGGGTGTGTGTGACAGATGACCCCTCT	2188	
Qy	2431	GCATGATTACTGACTACATGAGAACGGGACCTCAACAGTTTCCACTGTGCCACAGC	2490	
Db	2187	GCATGATCAACAGACTACATGAGAACGGGCGATTGAAACAGTTTCCATGTGCCCGCAGC	2248	
Qy	2491	TGGAGACAAAGGACGACGGAGGGGCCCTTGGGGACGGGACAGGCTGCGACGGGGCCACCA	2558	
Db	2247	TGGAAACAAAGGACACTAGGGGCGCTCTGTGGGACACAGATCTGACACAGGGGCCACAA	2308	
Qy	2551	TGAGTACCCAAATCTGTGTGATTTGGGACCCCAAGATCGCTCCCGGACAGCCCTATTTCG	2610	
Db	2307	TGAGTACCCCAATCTGTTCACATGGGGGCCCAAGATCGCTCTGGACATGCTTATCTCG	2366	
Qy	2611	CCACATCACTTTGTATCATCGGACCTGGCCACGGGAACTGCTTATGTTGGGAAAT	2670	
Db	2367	CCAGCTTAATCTTTGTGATGGGACCTGGCCACCGGAACTCTGTTGGGAAAT	2428	
Qy	2671	TCACCATCAAAATGCGAGACTTTGGCATGAGCCGGAACCTTATGCTGGGACTATTACC	2730	
Db	2427	TCACCATCAAAATGCGGACTTTGGCATGAGCCGGAATCTTACCTGGGGATTATTACC	2488	
Qy	2731	GTGTCCAGGGCGGGAGTGTGCGCATGCGGTGGAGTGGGCTGGAGTCAATCCATAG	2798	
Db	2487	GTGTCCAGGGCGGGAGTGTGCGCATGAGTGGATGGCTTGGAGTCAATCCATAG	2546	
Qy	2791	GGAAATTCACGACTGCGAGTACCTGTGGGACCTTTGATGTGACCCCTGTGGAGTGTGTA	2850	
Db	2547	GGAAATTCACAACAGCAGTGTGATTTGGGCTTCCGAGTGAACCTGTGGAGTGTGTA	2606	
Qy	2851	TGCTCTGTAGGGGCCAGCCCTTTGGGACTCACGACGACAGTCAATCGAAGACGG	2910	
Db	2607	TGCTCTGTAGGGTCCACGCCCTTTGGGAGCTTACAGATGAGAGTTATCGAATTCGG	2666	
Qy	2911	GGGAGTTTCCGGGAGACAGGGCGGAGGTGTACGTGCCGGCGCGCTGCTCAGCG	2970	
Db	2667	GGGAGTTTCCGGGAGACAGGGCGGAGGTGTACTGTGTCCAGGCCACCGCTCAGCG	2788	
Qy	2971	AGGGCTTATGAGCTGATGCTTGTGCTGAGAGCGGGAAGTCTGAGCAGCACCACT	3030	
Db	2727	AGACCTGTATGAGCTATGCTTCCGTTGTGAGCGGGAGGCCAGACAGCGCGCTCT	2786	
Qy	3031	TTTCCAGCTGATCGTCTCTGCGAGAGGATGCACTCAACAGGTGTGATCACATC	3090	
Db	2787	TTCGCCACCTTCATCGGTTCTCTGCGAGTATGCTCAACAGGTGTAACTCAGAGCC	2846	
Qy	3091	CAGGTGCCCCCTGCCCTAGGGAAGTGAATCCAGGGGAAGCCAGTGAACCTTAAACAGAGGA	3149	
Db	2847	CGGACGCCCTTTCCCAATGGGAAGCATCCAGGGGAAGC--TGAGTCTGAAACCCAGGAA	2904	
Qy	3150	CACATGACACCTTGCCCTTCCCTCCACAGACCCATCAGCTCTAATAGAGCAGTGA	3209	
Db	2905	CGCATGGCACCGGACCCACCGCTGTCCATCACTTGGC-----CATGCCAAGAGGAGTGT	2960	
Qy	3210	GACTGACAGTGGCTGGGCCACCCAGGAGTGTATGCCCCCTTCTCCCTCTTGACAC	3269	
Db	2961	CTTGTGCGGTGGGCTGGGCTGCGCCGAGGAGCATACACACT-----	3005	
Qy	3270	ACTGTACGTCCCTCTCTCTTCTTCTTCCCTCTTGAAGCCCTGTGGCCACCCACTGTGT	3329	
Db	3006	-----CCTTTCCTGTTTCTTCTTCCATCTGCCAAGTGTCCACCCACCACTGTGC	3054	
Qy	3330	CTGTGATGGATCTCTCACCTCTCTATGCCATCTCTTGGGGAAGGTGGGGAAGAA	3389	
Db	3055	CTGTGATGGATCTCTGCTCTGACTTCTTCCACTATCTCTTGGGGAAGAACGGGGGAA	3114	
Qy	3390	ATATAGATAGACCTGGACATGGCCATTGGAGACCTGGGCCCCACTGGACAACATG	3449	


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Db 3115 ATGCTGGAGTACTGGACA-----AGGCCCACTGGACAACACTG 3153
OY 3450 ATTCTGGAGAGTGGCTGGCCCCAGCTTCTCTCCCTGCACACACTGGACCCACT 3509
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Db 3154 GTTCCGGAAGGTGAGTGCCCC--CAGCTTCTCTGTGCACACTGGAGCCGCC 3211
OY 3510 GGCTGGAATCTG-6GGGTGAGAGGACAAGAAGAGAAATGTTCTGTGCTG 3568
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Db 3212 ACTGTGAATTAAGAGGGGTGAGGGGACAAGAGAG-----GCCAA 3251
OY 3569 CTCCTGACTTGTCCCTCAGCTTGGGCTTCTCTCTCCATCAGCTGAACACTGACCT 3628
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Db 3252 CCCCTACACCGGGTCCAGCCCTGCTCTCTCTCCGCCCTGACACACTGGACCT 3311
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OY 3683 TAGTAGAACTTCTTAAGCTATAGCTTCTGTGAGTAAATATGGATTGGGGGAA 3742
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OY 3743 AGAGGAGCAACGGCCATAGCCTTGGGGTGGACATCTCTAGTGTAGCTGCCACATGA 3802
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Db 3429 AGAGGGAGCAATAGCTTGAGGC--TGGGGGTGGGATTTCTATTGACTACACATGG 3486
OY 3803 TTTTCTATATCAGTCTGGGTTTGTACATTTT---GGGGGAGAGACACAGATTTTA 3859
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Db 3547 CACTAATATATGACCTAGCCTTAGGCGAATTTAATCCCTGCTAGGCAAGTAATAT 3606
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